



SEQUENCE LISTING

<110> KROHN, KAI
HEINO, MAARIT
PETERSON, PART
SCOTT, HAMISH S
ANTONARAKIS, STYLIANOS E
LALIOI, MARIA D
SHIMIZU, NOBUYOSHI D
KUDOH, JUN D

D1 <120> NOVEL GENE DEFECTIVE IN APECED AND ITS USE

<130> U 012653-9

<140> 09/508,658

<141> 2000-11-03

<150> PCT/FI98/00749

<151> 1998-09-23

<150> 973762

<151> 1997-09-23

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<170> .PatentIn version 3.1

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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Kai Krohn, et al.

Serial No.: 09/508,658

Group No.: 1634

Filed: November 3, 2000

Examiner.: Diana B. Johannsen

For: NOVEL GENE DEFECTIVE IN APECED AND ITS USE

Attorney Docket No.: U 012653-9

Assistant Commissioner of Patents
Washington, D.C. 20231

AMENDMENT

Please replace the sequence listing on file in this application with the attached sequence listing. Support for SEQ ID NO: 3 to 7 is found in Figure 5 and on page 6, lines 4-9 of the specification.

Respectfully submitted,



Janet I. Cord
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26 West 61st Street
New York, NY 10023
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CERTIFICATE OF MAILING /TRANSMISSION(37 CFR 1.8a)

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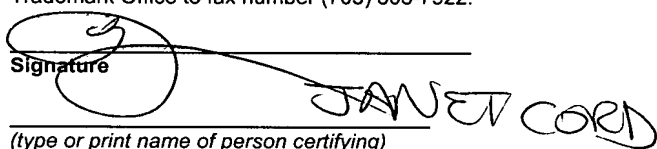
FACSIMILE

☐ transmitted by facsimile to the Patent and Trademark Office to fax number (703) 308-7922.



Signature

Date: January 15, 2003



(type or print name of person certifying)



SEQUENCE LISTING

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SCOTT, HAMISH S
ANTONARAKIS, STYLIANOS E
LALIOI, MARIA D
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KUDOH, JUN D

<120> NOVEL GENE DEFECTIVE IN APECED AND ITS USE

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Gln	Pro	Arg	Ala	Glu	Glu	Pro	Arg	Pro	Gln	Glu	Pro	Pro	Val	Glu	Thr	
	350					355					360					
ccg	ctc	ccc	ccg	ggg	ctt	agg	tcg	gcg	gga	gag	gag	gta	aga	ggg	cca	1276
Pro	Leu	Pro	Pro	Gly	Leu	Arg	Ser	Ala	Gly	Glu	Glu	Val	Arg	Gly	Pro	
365				370					375						380	
cct	ggg	gaa	ccc	cta	gcc	ggc	atg	gac	acg	act	ctt	gtc	tac	aag	cac	1324
Pro	Gly	Glu	Pro	Leu	Ala	Gly	Met	Asp	Thr	Thr	Leu	Val	Tyr	Lys	His	
			385					390						395		
ctg	ccg	gct	ccg	cct	tct	gca	gcc	ccg	ctg	cca	ggg	ctg	gac	tcc	tcg	1372
Leu	Pro	Ala	Pro	Pro	Ser	Ala	Ala	Pro	Leu	Pro	Gly	Leu	Asp	Ser	Ser	
			400					405					410			
gcc	ctg	cac	ccc	cta	ctg	tgt	gtg	ggg	cct	gag	ggg	cag	cag	aac	ctg	1420
Ala	Leu	His	Pro	Leu	Leu	Cys	Val	Gly	Pro	Glu	Gly	Gln	Gln	Asn	Leu	
	415					420						425				
gct	cct	ggg	gcg	cgt	tgc	ggg	gtg	tgc	gga	gat	ggg	acg	gac	gtg	ctg	1468
Ala	Pro	Gly	Ala	Arg	Cys	Gly	Val	Cys	Gly	Asp	Gly	Thr	Asp	Val	Leu	
	430				435						440					
cgg	tgt	act	cac	tgc	gcc	gct	gcc	ttc	cac	tgg	cgc	tgc	cac	ttc	cca	1516
Arg	Cys	Thr	His	Cys	Ala	Ala	Ala	Phe	His	Trp	Arg	Cys	His	Phe	Pro	
445				450				455							460	
gcc	ggc	acc	tcc	cgg	ccc	ggg	acg	ggc	ctg	cgc	tgc	aga	tcc	tgc	tca	1564
Ala	Gly	Thr	Ser	Arg	Pro	Gly	Thr	Gly	Leu	Arg	Cys	Arg	Ser	Cys	Ser	
			465					470						475		
gga	gac	gtg	acc	cca	gcc	cct	gtg	gag	ggg	gtg	ctg	gcc	ccc	agc	ccc	1612
Gly	Asp	Val	Thr	Pro	Ala	Pro	Val	Glu	Gly	Val	Leu	Ala	Pro	Ser	Pro	
			480				485						490			

gcc cgc ctg gcc cct ggg cct gcc aag gat gac act gcc agt cac gag 1660
Ala Arg Leu Ala Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu
495 500 505

ttc	gat	ggc	atc	ctg	cag	tgg	gcc	atc	cag	agc	atg	gcc	cgt	ccg	gcg	1756
Phe	Asp	Gly	Ile	Leu	Gln	Trp	Ala	Ile	Gln	Ser	Met	Ala	Arg	Pro	Ala	
525					530					535					540	

tgctgagaag gacacctcct tcctcagtcg tggaagccgg ccggctggga tcaagaaggg 1871

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Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
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Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
35 40 45

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65 70 75 80

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
 100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
 115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
 130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
 145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
 180 185 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
 210 215 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
 225 230 235 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
 245 250 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
 260 265 270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
 275 280 285

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
 290 295 300

Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
 305 310 315 320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg

325

330

335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
 340 345 350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
 355 360 365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
 370 375 380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
 385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
 405 410 415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
 420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
 435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
 450 455 460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
 465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
 485 490 495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
 500 505 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
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Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
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Ser
 545

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Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile
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Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys
35 40

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Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His Cys
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Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser Arg
20 25 30

Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys
35 40

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Pro Glu Gly Lys Trp Ser Cys Pro His Cys
35 40

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Pro Asn Gly Glu Trp Leu Cys Pro Arg Cys
35 40

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Pro Lys Val Phe His Leu Ser Cys His Val Pro Thr Leu Thr Asn Phe
20 25 30

Pro Ser Gly Glu Trp Ile Cys Thr Phe Cys
35 40